

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: BAICHWAL, VIJAY R  
HUANG, JIANING  
HSU, HAILING  
GOEDDEL, DAVID V

5 (ii) TITLE OF INVENTION: RIP: NOVEL HUMAN PROTEIN INVOLVED IN  
TUMOR NECROSIS FACTOR SIGNAL TRANSDUCTION, AND SCREENING  
ASSAYS

10 (iii) NUMBER OF SEQUENCES: 2

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP  
(B) STREET: 75 DENISE DRIVE  
(C) CITY: HILLSBOROUGH  
15 (D) STATE: CALIFORNIA  
(E) COUNTRY: USA  
(F) ZIP: 94010

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
20 (B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:  
25 (B) FILING DATE:  
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: OSMAN, RICHARD A.  
(B) REGISTRATION NUMBER: 36,627  
30 (C) REFERENCE/DOCKET NUMBER: T95-006-1

(ix) TELECOMMUNICATION INFORMATION:

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35 (B) TELEFAX: (650) 343-4342

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2016 base pairs  
(B) TYPE: nucleic acid  
40 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS  
45 (B) LOCATION: 1..2013

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATG	CAA	CCA	GAC	ATG	TCC	TTG	AAT	GTC	ATT	AAG	ATG	AAA	TCC	AGT	GAT		48	
Met	Gln	Pro	Asp	Met	Ser	Leu	Asn	Val	Ile	Lys	Met	Lys	Ser	Ser	Asp			
1	5								10						15			
5	TTC	CTG	GAG	AGT	GCA	GAA	CTG	GAC	AGC	GGA	GGC	TTT	GGG	AAG	GTG	TCT		96
	Phe	Leu	Glu	Ser	Ala	Glu	Leu	Asp	Ser	Gly	Gly	Phe	Gly	Lys	Val	Ser		
									20			25			30			
10	CTG	TGT	TTC	CAC	AGA	ACC	CAG	GGA	CTG	ATG	ATC	ATG	AAA	ACA	GTG	TAC		144
	Leu	Cys	Phe	His	Arg	Thr	Gln	Gly	Leu	Met	Ile	Met	Lys	Thr	Val	Tyr		
									35			40			45			
15	AAG	GGG	CCC	AAC	TGC	ATT	GAG	CAC	AAT	GAG	GCC	CTC	TTG	GAG	GAG	GCG		192
	Lys	Gly	Pro	Asn	Cys	Ile	Glu	His	Asn	Glu	Ala	Leu	Leu	Glu	Glu	Ala		
									50			55			60			
20	AAG	ATG	ATG	AAC	AGA	CTG	AGA	CAC	AGC	CGG	GTG	GTG	AAG	CTC	CTG	GGC		240
	Lys	Met	Met	Asn	Arg	Leu	Arg	His	Ser	Arg	Val	Val	Lys	Leu	Leu	Gly		
									65			70			75		80	
25	GTC	ATC	ATA	GAG	GAA	GGG	AAG	TAC	TCC	CTG	GTG	ATG	GAG	TAC	ATG	GAG		288
	Val	Ile	Ile	Glu	Glu	Gly	Lys	Tyr	Ser	Leu	Val	Met	Glu	Tyr	Met	Glu		
									85			90			95			
30	AAG	GGC	AAC	CTG	ATG	CAC	GTG	CTG	AAA	GCC	GAG	ATG	AGT	ACT	CCG	CTT		336
	Lys	Gly	Asn	Leu	Met	His	Val	Leu	Lys	Ala	Glu	Met	Ser	Thr	Pro	Leu		
									100			105			110			
35	TCT	GTA	AAA	GGA	AGG	ATA	ATT	TTG	GAA	ATC	ATT	GAA	GGA	ATG	TGC	TAC		384
	Ser	Val	Lys	Gly	Arg	Ile	Ile	Leu	Glu	Ile	Ile	Glu	Gly	Met	Cys	Tyr		
									115			120			125			
40	TTA	CAT	GGA	AAA	GGC	GTG	ATA	CAC	AAG	GAC	CTG	AAG	CCT	GAA	AAT	ATC		432
	Leu	His	Gly	Lys	Gly	Val	Ile	His	Lys	Asp	Leu	Lys	Pro	Glu	Asn	Ile		
									130			135			140			
45	CTT	GTT	GAT	AAT	GAC	TTC	CAC	ATT	AAG	ATC	GCA	GAC	CTC	GGC	CTT	GCC		480
	Leu	Val	Asp	Asn	Asp	Phe	His	Ile	Lys	Ile	Ala	Asp	Leu	Gly	Leu	Ala		
									145			150			155		160	
50	TCC	TTT	AAG	ATG	TGG	AGC	AAA	CTG	AAT	AAT	GAA	GAG	CAC	AAT	GAG	CTG		528
	Ser	Phe	Lys	Met	Trp	Ser	Lys	Leu	Asn	Asn	Glu	Glu	His	Asn	Glu	Leu		
									165			170			175			
55	AGG	GAA	GTG	GAC	GGC	ACC	GCT	AAG	AAG	AAT	GGC	GGC	ACC	CTC	TAC	TAC		576
	Arg	Glu	Val	Asp	Gly	Thr	Ala	Lys	Lys	Asn	Gly	Gly	Thr	Leu	Tyr	Tyr		
									180			185			190			
60	ATG	CGC	CCC	GAG	CAC	CTG	AAT	GAC	GTC	AAC	GCA	AAG	CCC	ACA	GAG	AAG		624
	Met	Ala	Pro	Glu	His	Leu	Asn	Asp	Val	Asn	Ala	Lys	Pro	Thr	Glu	Lys		
									195			200			205			
65	TCG	GAT	GTG	TAC	AGC	TTT	GCT	GTA	GTC	CTC	TGG	GCG	ATA	TTT	GCA	AAT		672
	Ser	Asp	Val	Tyr	Ser	Phe	Ala	Val	Leu	Trp	Ala	Ile	Phe	Ala	Asn			
									210			215			220			
70	AAG	GAG	CCA	TAT	GAA	AAT	GCT	ATC	TGT	GAG	CAG	CAG	TTG	ATA	ATG	TGC		720

Lys	Glu	Pro	Tyr	Glu	Asn	Ala	Ile	Cys	Glu	Gln	Gln	Leu	Ile	Met	Cys		
225				230					235					240			
ATA	AAA	TCT	GGG	AAC	AGG	CCA	GAT	GTG	GAT	GAC	ATC	ACT	GAG	TAC	TGC	768	
Ile	Lys	Ser	Gly	Asn	Arg	Pro	Asp	Val	Asp	Asp	Ile	Thr	Glu	Tyr	Cys		
5				245					250				255				
CCA	AGA	GAA	ATT	ATC	AGT	CTC	ATG	AAG	CTC	TGC	TGG	GAA	GCG	AAT	CCG	816	
Pro	Arg	Glu	Ile	Ile	Ser	Leu	Met	Lys	Leu	Cys	Trp	Glu	Ala	Asn	Pro		
			260					265			270						
GAA	GCT	CGG	CCG	ACA	TTT	CCT	GGC	ATT	GAA	GAA	AAA	TTT	AGG	CCT	TTT	864	
10	Glu	Ala	Arg	Pro	Thr	Phe	Pro	Gly	Ile	Glu	Glu	Lys	Phe	Arg	Pro	Phe	
	275			280					285								
TAT	TTA	AGT	CAA	TTA	GAA	GAA	AGT	GTA	GAA	GAG	GAC	GTG	AAG	AGT	TTA	912	
Tyr	Leu	Ser	Gln	Leu	Glu	Glu	Ser	Val	Glu	Glu	Asp	Val	Lys	Ser	Leu		
	290			295				300									
15	AAG	AAA	GAG	TAT	TCA	AAC	GAA	AAT	GCA	GTT	GTG	AAG	AGA	ATG	CAG	TCT	960
Lys	Lys	Glu	Tyr	Ser	Asn	Glu	Asn	Ala	Val	Val	Lys	Arg	Met	Gln	Ser		
	305			310				315			320						
CTT	CAA	CTT	GAT	TGT	GTG	GCA	GTA	CCT	TCA	AGC	CGG	TCA	AAT	TCA	GCC	1008	
Leu	Gln	Leu	Asp	Cys	Val	Ala	Val	Pro	Ser	Ser	Arg	Ser	Asn	Ser	Ala		
20				325				330			335						
ACA	GAA	CAG	CCT	GGT	TCA	CTG	CAC	AGT	TCC	CAG	GGA	CTT	GGG	ATG	GGT	1056	
Thr	Glu	Gln	Pro	Gly	Ser	Leu	His	Ser	Ser	Gln	Gly	Leu	Gly	Met	Gly		
	340			345				350									
CCT	GTG	GAG	GAG	TCC	TGG	TTT	GCT	CCT	TCC	CTG	GAG	CAC	CCA	CAA	GAA	1104	
25	Pro	Val	Glu	Glu	Ser	Trp	Phe	Ala	Pro	Ser	Leu	Glu	His	Pro	Gln	Glu	
	355			360				365									
GAG	AAT	GAG	CCC	AGC	CTG	CAG	AGT	AAA	CTC	CAA	GAC	GAA	GCC	AAC	TAC	1152	
Glu	Asn	Glu	Pro	Ser	Leu	Gln	Ser	Lys	Leu	Gln	Asp	Glu	Ala	Asn	Tyr		
	370			375				380									
CAT	CTT	TAT	GGC	AGC	CGC	ATG	GAC	AGG	CAG	ACG	AAA	CAG	CAG	CCC	AGA	1200	
His	Leu	Tyr	Gly	Ser	Arg	Met	Asp	Arg	Gln	Thr	Lys	Gln	Gln	Pro	Arg		
	385			390				395			400						
CAG	AAT	GTG	GCT	TAC	AAC	AGA	GAG	GAG	GAA	AGG	AGA	CGC	AGG	GTC	TCC	1248	
Gln	Asn	Val	Ala	Tyr	Asn	Arg	Glu	Glu	Glu	Arg	Arg	Arg	Arg	Val	Ser		
35				405				410			415						
CAT	GAC	CCT	TTT	GCA	CAG	CAA	AGA	CCT	TAC	GAG	AAT	TTT	CAG	AAT	ACA	1296	
His	Asp	Pro	Phe	Ala	Gln	Gln	Arg	Pro	Tyr	Glu	Asn	Phe	Gln	Asn	Thr		
	420			425				430									
GAG	GGA	AAA	GGC	ACT	GTT	TAT	TCC	AGT	GCA	GCC	AGT	CAT	GGT	AAT	GCA	1344	
40	Glu	Gly	Lys	Gly	Thr	Val	Tyr	Ser	Ser	Ala	Ala	Ser	His	Gly	Asn	Ala	
	435			440				445									
GTG	CAC	CAG	CCC	TCA	GGG	CTC	ACC	AGC	CAA	CCT	CAA	GTA	CTG	TAT	CAG	1392	
Val	His	Gln	Pro	Ser	Gly	Leu	Thr	Ser	Gln	Pro	Gln	Val	Leu	Tyr	Gln		
	450			455				460									

AAC AAT GGA TTA TAT AGC TCA CAT GGC TTT GGA AGA AGA CCA CTG GAT			1440
Asn Asn Gly Leu Tyr Ser Ser His Gly Phe Gly Thr Arg Pro Leu Asp			
465	470	475	480
CCA GGA ACA GCA GGT CCC AGA GTT TGG TAC AGG CCA ATT CCA AGT CAT			1488
Pro Gly Thr Ala Gly Pro Arg Val Trp Tyr Arg Pro Ile Pro Ser His			
5	485	490	495
ATG CCT AGT CTG CAT AAT ATC CCA GTG CCT GAG ACC AAC TAT CTA GGA			1536
Met Pro Ser Leu His Asn Ile Pro Val Pro Glu Thr Asn Tyr Leu Gly			
10	500	505	510
AAT ACA CCC ACC ATG CCA TTC AGC TCC TTG CCA CCA ACA GAT GAA TCT			1584
Asn Thr Pro Thr Met Pro Phe Ser Ser Leu Pro Pro Thr Asp Glu Ser			
515	520	525	
ATA AAA TAT ACC ATA TAC AAT AGT ACT GGC ATT CAG ATT GGA GCC TAC			1632
Ile Lys Tyr Thr Ile Tyr Asn Ser Thr Gly Ile Gln Ile Gly Ala Tyr			
15	530	535	540
AAT TAT ATG GAG ATT GGT GGG ACG AGT TCA TCA CTA CTA GAC AGC ACA			1680
Asn Tyr Met Glu Ile Gly Gly Thr Ser Ser Ser Leu Leu Asp Ser Thr			
545	550	555	560
AAT ACG AAC TTC AAA GAA GAG CCA GCT GCT AAG TAC CAA GCT ATC TTT			1728
20	Asn Thr Asn Phe Lys Glu Glu Pro Ala Ala Lys Tyr Gln Ala Ile Phe		
565	570	575	
GAT AAT ACC ACT AGT CTG ACG GAT AAA CAC CTG GAC CCA ATC AGG GAA			1776
Asp Asn Thr Thr Ser Leu Thr Asp Lys His Leu Asp Pro Ile Arg Glu			
580	585	590	
AAT CTG GGA AAG CAC TGG AAA AAC TGT GCC CGT AAA CTG GGC TTC ACA			1824
25	Asn Leu Gly Lys His Trp Lys Asn Cys Ala Arg Lys Leu Gly Phe Thr		
595	600	605	
CAG TCT CAG ATT GAT GAA ATT GAC CAT GAC TAT GAG CGA GAT GGA CTG			1872
Gln Ser Gln Ile Asp Glu Ile Asp His Asp Tyr Glu Arg Asp Gly Leu			
30	610	615	620
AAA GAA AAG GTT TAC CAG ATG CTC CAA AAG TGG GTG ATG AGG GAA GGC			1920
Lys Glu Lys Val Tyr Gln Met Leu Gln Lys Trp Val Met Arg Glu Gly			
625	630	635	640
ATA AAG GGA GCC ACG GTG GGG AAG CTG GCC CAG GCG CTC CAC CAG TGT			1968
35	Ile Lys Gly Ala Thr Val Gly Lys Leu Ala Gln Ala Leu His Gln Cys		
645	650	655	
TCC AGG ATC GAC CTT CTG AGC AGC TTG ATT TAC GTC AGC CAG AAC			2013
Ser Arg Ile Asp Leu Leu Ser Ser Leu Ile Tyr Val Ser Gln Asn			
660	665	670	
40	TAA		2016

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 671 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

5 Met Gln Pro Asp Met Ser Leu Asn Val Ile Lys Met Lys Ser Ser Asp  
1 5 10 15  
Phe Leu Glu Ser Ala Glu Leu Asp Ser Gly Gly Phe Gly Lys Val Ser  
20 25 30  
Leu Cys Phe His Arg Thr Gln Gly Leu Met Ile Met Lys Thr Val Tyr  
10 35 40 45  
Lys Gly Pro Asn Cys Ile Glu His Asn Glu Ala Leu Leu Glu Glu Ala  
50 55 60  
Lys Met Met Asn Arg Leu Arg His Ser Arg Val Val Lys Leu Leu Gly  
65 70 75 80  
15 Val Ile Ile Glu Glu Gly Lys Tyr Ser Leu Val Met Glu Tyr Met Glu  
85 90 95  
Lys Gly Asn Leu Met His Val Leu Lys Ala Glu Met Ser Thr Pro Leu  
100 105 110  
Ser Val Lys Gly Arg Ile Ile Leu Glu Ile Ile Glu Gly Met Cys Tyr  
20 115 120 125  
Leu His Gly Lys Gly Val Ile His Lys Asp Leu Lys Pro Glu Asn Ile  
130 135 140  
Leu Val Asp Asn Asp Phe His Ile Lys Ile Ala Asp Leu Gly Leu Ala  
145 150 155 160  
25 Ser Phe Lys Met Trp Ser Lys Leu Asn Asn Glu Glu His Asn Glu Leu  
165 170 175  
Arg Glu Val Asp Gly Thr Ala Lys Lys Asn Gly Gly Thr Leu Tyr Tyr  
180 185 190  
Met Ala Pro Glu His Leu Asn Asp Val Asn Ala Lys Pro Thr Glu Lys  
30 195 200 205  
Ser Asp Val Tyr Ser Phe Ala Val Val Leu Trp Ala Ile Phe Ala Asn  
210 215 220  
Lys Glu Pro Tyr Glu Asn Ala Ile Cys Glu Gln Gln Leu Ile Met Cys  
225 230 235 240  
35 Ile Lys Ser Gly Asn Arg Pro Asp Val Asp Asp Ile Thr Glu Tyr Cys  
245 250 255  
Pro Arg Glu Ile Ile Ser Leu Met Lys Leu Cys Trp Glu Ala Asn Pro  
260 265 270  
Glu Ala Arg Pro Thr Phe Pro Gly Ile Glu Glu Lys Phe Arg Pro Phe  
40 275 280 285  
Tyr Leu Ser Gln Leu Glu Glu Ser Val Glu Glu Asp Val Lys Ser Leu  
290 295 300  
Lys Lys Glu Tyr Ser Asn Glu Asn Ala Val Val Lys Arg Met Gln Ser  
305 310 315 320

	Leu Gln Leu Asp Cys Val Ala Val Pro Ser Ser Arg Ser Asn Ser Ala		
	325	330	335
	Thr Glu Gln Pro Gly Ser Leu His Ser Ser Gln Gly Leu Gly Met Gly		
	340	345	350
5	Pro Val Glu Glu Ser Trp Phe Ala Pro Ser Leu Glu His Pro Gln Glu		
	355	360	365
	Glu Asn Glu Pro Ser Leu Gln Ser Lys Leu Gln Asp Glu Ala Asn Tyr		
	370	375	380
	His Leu Tyr Gly Ser Arg Met Asp Arg Gln Thr Lys Gln Gln Pro Arg		
10	385	390	395
	Gln Asn Val Ala Tyr Asn Arg Glu Glu Arg Arg Arg Arg Val Ser		
	405	410	415
	His Asp Pro Phe Ala Gln Gln Arg Pro Tyr Glu Asn Phe Gln Asn Thr		
	420	425	430
15	Glu Gly Lys Gly Thr Val Tyr Ser Ser Ala Ala Ser His Gly Asn Ala		
	435	440	445
	Val His Gln Pro Ser Gly Leu Thr Ser Gln Pro Gln Val Leu Tyr Gln		
	450	455	460
	Asn Asn Gly Leu Tyr Ser Ser His Gly Phe Gly Thr Arg Pro Leu Asp		
20	465	470	475
	Pro Gly Thr Ala Gly Pro Arg Val Trp Tyr Arg Pro Ile Pro Ser His		
	485	490	495
	Met Pro Ser Leu His Asn Ile Pro Val Pro Glu Thr Asn Tyr Leu Gly		
	500	505	510
25	Asn Thr Pro Thr Met Pro Phe Ser Ser Leu Pro Pro Thr Asp Glu Ser		
	515	520	525
	Ile Lys Tyr Thr Ile Tyr Asn Ser Thr Gly Ile Gln Ile Gly Ala Tyr		
	530	535	540
	Asn Tyr Met Glu Ile Gly Thr Ser Ser Ser Leu Leu Asp Ser Thr		
30	545	550	555
	Asn Thr Asn Phe Lys Glu Glu Pro Ala Ala Lys Tyr Gln Ala Ile Phe		
	565	570	575
	Asp Asn Thr Thr Ser Leu Thr Asp Lys His Leu Asp Pro Ile Arg Glu		
	580	585	590
35	Asn Leu Gly Lys His Trp Lys Asn Cys Ala Arg Lys Leu Gly Phe Thr		
	595	600	605
	Gln Ser Gln Ile Asp Glu Ile Asp His Asp Tyr Glu Arg Asp Gly Leu		
	610	615	620
	Lys Glu Lys Val Tyr Gln Met Leu Gln Lys Trp Val Met Arg Glu Gly		
40	625	630	635
	Ile Lys Gly Ala Thr Val Gly Lys Leu Ala Gln Ala Leu His Gln Cys		
	645	650	655
	Ser Arg Ile Asp Leu Leu Ser Ser Leu Ile Tyr Val Ser Gln Asn		
	660	665	670